Amendments to the Specification

Please insert a new paragraph in the Specification before the Background to the Invention (before line 4):

This application claims priority from USSN 60/524,645 filed on November 25th, 2003 and incorporated by reference in its entirety.

Please replace the paragraph at page 5, lines 10 to 23, with the following amended paragraph:

Figure 2 A: Comparison of the amino acid sequences of the nasturtium FAE homolog (NasFAE; accession no. AY0826190, SEQ ID NO:22) with fatty acid elongase1 (FAE1) and related 3-ketoacyl-CoA synthases from other plant species. The alignment contains the sequences of the corn (ZeaFAE, SEQ ID NO:30), *Limnanthes* (LimFAE,SEQ ID NO:31), jojoba (SimFAE, SEQ ID NO:32), *Arabidopis* (AraFAE, SEQ ID NO:26) *Brassica* (BraFAE, SEQ ID NO:35) and two *Arabidopis* 3-ketoacyl-CoA synthases associated with wax synthesis (AraKCS, SEQ ID NO:33; AraCUT, SEQ ID NO:34). The GenBank Accession numbers for the sequences shown are AJ292770 (ZeaFAE), AF247134 (LimFAE), U37088 (SimFAE), AF053345 (AraKCS), AF129511 (AraACUT), U29142 (AraFAE), AF009563 (BraFAE). Conserved cysteine and histidine residues are labeled with diamonds and triangles, respectively. Tyrosine at position 429 in the nasturtium FAE polypeptide is indicated by an asterisk. **B:** Dendrogram of the 3-ketoacyl-CoA synthase gene family based on the amino acid sequences. The alignment was carried out by the Clustal W method using Lasergene analysis software (DNAStar, Madison, WI) GenBank accession numbers: AF247134 (LimFAE), U37088 (SimFAE), AY082610 (NasFAE), AJ292770 (ZeaFAE), AF053345 (AraKCS), U29142 (AraFAE), AF009563 (BraFAE), AF129511 (AraCUT).

Please replace the paragraph bridging page 12, line 34 to page 13, line 5, with the following amended paragraph:

A hydropathy analysis (Kyte-Doolittle) of the amino acid sequence of the *T. majus* FAE revealed several hydrophobic domains (Fig. 3A). Protein analyses with the TMAP algorithm (Person and Argos, 1994) predicted two *N*-terminal transmembrane domains, the first

corresponding to amino-acid residues 35-55, and the second spanning residues 68-88 (Fig 3B). Like other elongase condensing enzymes, the *T. majus* FAE lacks *N*-terminal signal sequences typically found for plastidial or mitochondrial-targeted plant enzymes. It also lacks a **K**X**K**XX (SEQ ID NO:28) or **KK**XX (SEQ ID NO:29) motif (X=any amino acid) often found at the *C*-terminus of proteins retained within ER membranes. Rather, it is a type IIIa protein, typically present on endoplasmic reticular membranes.

Please replace the paragraph bridging page 24, lines 22 to 27, with the following amended paragraph:

All field trials were conducted by the Saskatchewan Wheat Pool at Rosthern, Saskatchewan (Saskatoon farmzone) in the two successive years. The first field trial growing season (26 May-21 Sept) exhibited 1519 growing degree days, 2309 crop heat units and 172.4 mm of precipitation accumulation. The second field trial growing season (26 May-21 Sept) exhibited 757 growing degree-days, 1278 crop heat units and 167.5 mm of precipitation accumulation (http://www.farmzone.com/report/climate.asp).